

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**





























Figure 1: Oxydative Phosphorylation Genes

Complex I	
NADH-ubiquinone oxidoreductase (MWFE)	-1.334
NADH-ubiquinone oxidoreductase (BB)	-1.264
NADH-ubiquinone oxidoreductase (SGDH)	-1.323
NADH-ubiquinone oxidoreductase (75kD)	-1.257
NADH-ubiquinone oxidoreductase (51kD)	-1.25
NADH-ubiquinone oxidoreductase (49kD)	-1.212
NADH-ubiquinone oxidoreductase (39kD)	-1.199
NADH-ubiquinone oxidoreductase (13kD)	-1.377
NADH-ubiquinone oxidoreductase (30kD)	-1.344
NADH-ubiquinone oxidoreductase (23kD)	-1.092
NADH-ubiquinone oxidoreductase (partial)	-1.162
NADH-ubiquinone oxidoreductase (9.6 kD)	-1.446
Complex II	
Succinate dehydrogenase-Flavoprotein	-1.265
Succinate dehydrogenase-iron-sulfur	-1.226
Succinate dehydrogenase, subunit C	-1.085
Succinate dehydrogenase subunit D	-1.108
Complex III	
Ubiquinol-CytC reductase-RISP	1.011
Ubiquinol-CytC reductase subunit I	-1.418
Ubiquinol-CytC reductase subunit II	-1.212
Cyt reductase-B5	-1.08
Ubiquinol-CytC reductase binding prot	-1.267
Ubiquinol-CytC reductase subunit VII	-1.372
CytC reductase subunit VIII	-1.372
Ubiquinol-CytC reductase (6.4 kD)	-1.195
Ubiquinol-CytC reductase (6.4 kD)	1.004
Cyt C1	-1.103
Complex IV	
Cyt C	-1.299
COX IV	-1.148
COX Va	-1.402
COX Vb	-1.278
COX VIa	-1.129
COX VIb	-1.331
COX VIb-2	-1.012
COX VIc	-1.353
COX VIIa-1	-1.314
COX VIIa2/liver	-1.417
COX VIIa-related	-1.129
COX VIIb	-1.58
COX VIIc	-1.13
COX VIII	-1.222
COX 17 homolog	-1.264
Complex V	
F(0)	
Subunit B	1.0566
Subunit C1	-1.148
Subunit C3	-1.627
Subunit D	-1.667
Subunit E	-1.191
Subunit F	-1.477
Subunit F6	-1.4
Subunit G	-1.152
F(0) to F(1)	
ATP synthase (OSCP)	-1.529
F(1)	
alpha chain	-1.383
gamma chain	-1.464
delta chain	-1.272

Legend

- ☒ upregulated in BD, $p \leq 0.02$
- ☒ upregulated in BD, $p \leq 0.05$
- ☒ downregulated in BD, $p \leq 0.02$
- ☒ downregulated in BD, $p \leq 0.05$
- ☐ No criteria met
- ☐ Not found

Figure 2 Ubiquitin/Proteasome Degradation

Proteasome 19 S (ATP dependent)			Proteasome 20S Catalytic Core				
 subunit 1	-1.363	 subunit 9	1.0256	 C2 (alpha 1)	-1.305	 C5 (beta 1)	-1.325
 subunit 2	-1.165	 subunit 10b	-1.486	 C3 (alpha 2)	-1.17	 C7 (beta 2)	-1.314
 subunit 3	-1.156	 subunit 11	-1.364	 C8 (alpha 3)	-1.393	 C10-II (beta 3)	-1.239
 subunit 4	-1.208	 subunit 12	-1.129	 C9 (alpha 4)	-1.228	 beta 4	-1.418
 subunit 5a	-1.215	 subunit 14	-1.302	 iota (alpha 6)	-1.379	 epsilon (beta 5)	-1.173
 subunit 5b	1.0723	 subunit p55	-1.112	 alpha 7	1.1047	 Delta (beta 6)	-1.19
 subunit 6a	-1.258	 subunit p40.5	-1.214			 Z (beta 7)	-1.204
 subunit 7	-1.202						

Legend







	upregulated in BD, p<=0.02
	upregulated in BD, p<=0.05
	downregulated in BD, p<=0.02
	downregulated in BD, p<=0.05
	No criteria met
	Not found

Figure 3

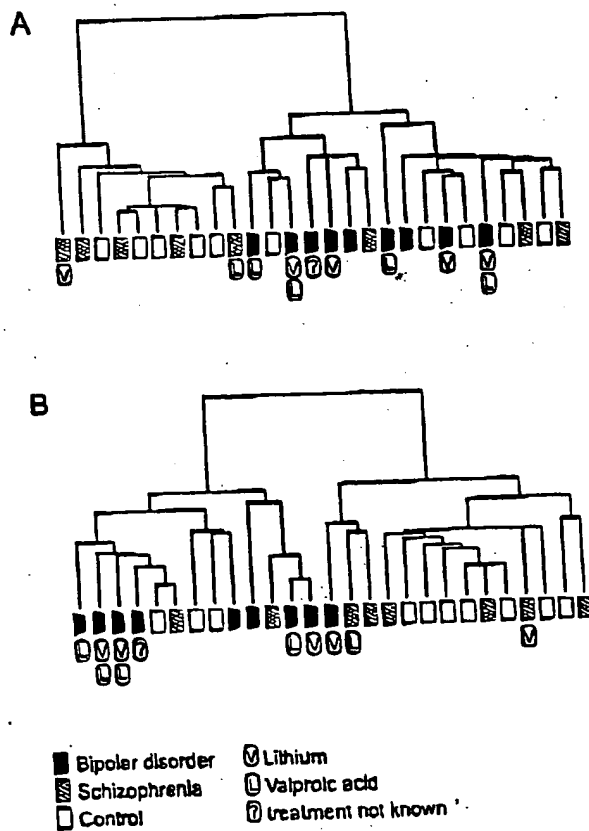


Figure 4

